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## **AMENDMENTS TO THE CLAIMS;**

This listing of claims will replace all prior versions and listing of the claims in the application:

## **LISTING OF THE CLAIMS:**

Claims 1-65 (canceled).

Claim 66. (currently amended) An in vitro method of making linear sequence variants from at least one heteroduplex polynucleotide where said heteroduplex has at least two non-complementary nucleotide base pairs separated by complementary nucleotide base pairs, said method comprising:

- a. preparing at least one heteroduplex polynucleotide;
- b. combining said heteroduplex polynucleotide with a <u>defined composition</u>

  <u>containing enzymes wherein the enzymes consist essentially of an effective amount of CEL</u>

  I, T4 DNA polymerase, and T4 DNA ligase; and
- c. allowing sufficient time for the percentage of complementarity to increase, wherein one or more sequence variants are made thereby increasing the diversity in a population of polynucleotides; and
- d. separating and recovering at least one sequence variant having a sequence different from either polynucleotide strand in said heteroduplex.

Claim 67. (currently amended) An in vitro method of making linear sequence variants from at least one heteroduplex polynucleotide wherein said heteroduplex has at least two

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non-complementary nucleotide base pairs separated by complementary nucleotide base pairs, said method comprising:

a. preparing at least one heteroduplex polynucleotide;

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- b. combining said heteroduplex polynucleotide with <u>a defined composition</u>

  <u>containing enzymes wherein the enzymes consist essentially of</u> an effective amount of an <u>agent or agents- enzyme or enzymes</u> with exonuclease activity, polymerase activity and a mismatch recognizing and mismatch directed endonuclease <u>that cleaves at the mismatched nucleotides</u>; and
- c. allowing sufficient time for the percentage of complementarity to increase, wherein at least one or more sequence variants are made thereby increasing diversity in a population of polynucleotides; and
- d. separating and recovering at least one sequence variant having a sequence different from either polynucleotide in the heteroduplex.

Claim 68. (currently amended) The method of claim 67 wherein said endonuclease is added first, the agent enzyme or enzymes having 3' to 5' exonuclease activity is added second, and the agent enzyme or enzymes having polymerase activity is added third.

Claim 69. (currently amended) The method of claim 67 wherein said agents enzymes having exonuclease activity, polymerase activity, and endonuclease are added concurrently.

Claim 70. (original) The method of claim 67 in step (b) further comprising ligase activity.

Claim 71. (original) The method of claim 69 further comprising a step of, (d) adding a ligase.

Claim 72. (original) The method of claim 70 wherein said ligase is T4 DNA ligase, E. coli

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DNA ligase, or Taq DNA ligase.

Claims 73-77 (canceled)

Claim 78. (original) The method of claim 67 wherein said agent with polymerase activity is T4 DNA polymerase.

Claim 79. (currently amended) The method of claim 67 wherein said agent enzyme with both polymerase activity and 3' to 5' exonuclease activity is T4 DNA polymerase, T7 DNA polymerase, E. coli Pol 1, or Pfu DNA polymerase.

Claim 80. (currently amended) The method of claim 67 wherein said agent enzyme with both polymerase activity and 5' to 3' exonuclease activity is E. coli Pol 1.

Claim 81. (previously presented) The method of claim 67 wherein said effective amount of said endonuclease, and exonuclease activity/polymerase activity and ligase activity are provided by CEL I, T4 DNA polymerase, and T4 DNA ligase.

Claim 82. (currently amended) The method of claim 67 wherein said effective amount of said endonuclease, and exonuclease activity/polymerase activity and ligase activity are provided by CEL I, T7 DNA polymerase, and T4 DNA ligase.

Claim 83. (previously presented) The method of claim 67 wherein an effective amount of said endonuclease, and exonuclease activity/polymerase activity and ligase activity are provided by T4 endonuclease VII, T4 DNA polymerase, and T4 DNA ligase.

Claim 84. (canceled)

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Claim 85. (original) The method of claim 67 wherein complementarity is complete yielding a homoduplex polynucleotide.

Claim 86. (canceled)

Claim 87. (currently amended) The method of claim 86 67 wherein at least 2 different polynucleotide sequence variants are formed and recovered.

Claim 88. (previously presented) The method of claim 67 further comprising screening or selecting a population of sequence variants for a desired functional property.

Claim 89. (previously presented) The method of claim 88 further comprising selecting a sequence variant that has a different desired function property from any parent polynucleotide.

Claim 90. (currently amended) The method of claim 86 67 wherein said at least one heteroduplex polynucleotide has at least three non-complementary nucleotide base pairs separated by complementary nucleotide base pairs and at least 4 different sequence variants made.